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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/051,311DATE: 02/05/2002
TIME: 16:57:39Input Set : A:\seqlist_0652.2290001
Output Set: N:\CRF3\02052002\J051311.raw**ENTERED**

3 <110> APPLICANT: Boehringer Ingelheim International GmbH
5 <120> TITLE OF INVENTION: Method for identifying compounds that modulate sister
6 chromatid separation
8 <130> FILE REFERENCE: 0652.2290001
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/051,311
C--> 11 <141> CURRENT FILING DATE: 2002-01-22
13 <150> PRIOR APPLICATION NUMBER: EP 01 101 252.3
14 <151> PRIOR FILING DATE: 2001-01-19
16 <150> PRIOR APPLICATION NUMBER: US 60/297,440
17 <151> PRIOR FILING DATE: 2001-06-13
19 <160> NUMBER OF SEQ ID NOS: 8
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 6668
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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30 <222> LOCATION: (1)..(144)
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (145)..(6507)
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43 accttcagcc ctcttccctt cctccagtta gcttcattaa caatcttctc taattgggtc 120
45 ccttttccct agctctccgg tgct atg agg agc ttc aaa aga gtc aac ttt 171
46 Met Arg Ser Phe Lys Arg Val Asn Phe
47 1 5
49 ggg act ctg cta agc agc cag aag gag gct gaa gag ttg ctg ccc gac 219
50 Gly Thr Leu Leu Ser Ser Gln Lys Glu Ala Glu Glu Leu Leu Pro Asp
51 10 15 20 25
53 ttg aag gag ttc ctg tcc aac cct cca gct ggt ttt ccc agc agc cga 267
54 Leu Lys Glu Phe Leu Ser Asn Pro Pro Ala Gly Phe Pro Ser Ser Arg
55 30 35 40
57 tct gat gct gag agg aga caa gct tgt gat gcc atc ctg agg gct tgc 315
58 Ser Asp Ala Glu Arg Arg Gln Ala Cys Asp Ala Ile Leu Arg Ala Cys
59 45 50 55
61 aac cag cag ctg act gct aag cta gct tgc cct agg cat ctg ggg agc 363
62 Asn Gln Gln Leu Thr Ala Lys Leu Ala Cys Pro Arg His Leu Gly Ser
63 60 65 70

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65 ctg ctg gag ctg gca gag ctg gcc tgt gat ggc tac tta gtg tct acc 411
66 Leu Leu Glu Leu Ala Glu Leu Ala Cys Asp Gly Tyr Leu Val Ser Thr
67      75      80      85
70 cca cag cgt cct ccc ctg tac ctg gaa cga att ctg ttt gtc tta ctg 459
71 Pro Gln Arg Pro Pro Leu Tyr Leu Glu Arg Ile Leu Phe Val Leu Leu
72 90      95      100      105
74 cgg aat gct gct gca caa gga agc cca gag gtc aca ctg cgc ctt gct 507
75 Arg Asn Ala Ala Ala Gln Gly Ser Pro Glu Val Thr Leu Arg Leu Ala
76      110      115      120
78 cag ccc ctg cat gcc tgc ttg gtg cag tgc tct cgc gag gct gct ccc 555
79 Gln Pro Leu His Ala Cys Leu Val Gln Cys Ser Arg Glu Ala Ala Pro
80      125      130      135
82 cag gac tat gag gcc gtg gct cgg ggc agc ttt tct ctg ctt tgg aag 603
83 Gln Asp Tyr Glu Ala Val Ala Arg Gly Ser Phe Ser Leu Leu Trp Lys
84      140      145      150
86 ggg gca gaa gcc ctg ttg gaa cgg cga gct gca ttt gca gct cgg ctg 651
87 Gly Ala Glu Ala Leu Leu Glu Arg Arg Ala Ala Phe Ala Ala Arg Leu
88      155      160      165
90 aag gcc ttg agc ttc cta gta ctg ttg gag gat gaa agt acc cct tgt 699
91 Lys Ala Leu Ser Phe Leu Val Leu Leu Glu Asp Glu Ser Thr Pro Cys
92 170      175      180      185
94 gag gtt cct cac ttt gct tct cca aca gcc tgt cga gcg gta gct gcc 747
95 Glu Val Pro His Phe Ala Ser Pro Thr Ala Cys Arg Ala Val Ala Ala
96      190      195      200
98 cat cag cta ttt gat gcc agt ggc cat ggt cta aat gaa gca gat gct 795
99 His Gln Leu Phe Asp Ala Ser Gly His Gly Leu Asn Glu Ala Asp Ala
100      205      210      215
102 gat ttc cta gat gac ctg ctg tcc agg cac gtg atc aga gcc ttg gtg 843
103 Asp Phe Leu Asp Asp Leu Leu Ser Arg His Val Ile Arg Ala Leu Val
104      220      225      230
106 ggt gag aga ggg agc tct tct ggg ctt ctt tct ccc cag agg gcc ctg 891
107 Gly Glu Arg Gly Ser Ser Ser Gly Leu Leu Ser Pro Gln Arg Ala Leu
108      235      240      245
110 tgc ctg ttg gag ctg acc ttg gaa cac tgc cgt cgc ttt tgc tgg agc 939
111 Cys Leu Leu Glu Leu Thr Leu Glu His Cys Arg Arg Phe Cys Trp Ser
112 250      255      260      265
114 cgc cac cat gac aaa gcc atc agc gca gtg gag aag gct cac agt tac 987
115 Arg His His Asp Lys Ala Ile Ser Ala Val Glu Lys Ala His Ser Tyr
116      270      275      280
118 cta agg aac acc aat cta gcc cct agc ctt cag cta tgt cag ctg ggg 1035
119 Leu Arg Asn Thr Asn Leu Ala Pro Ser Leu Gln Leu Cys Gln Leu Gly
120      285      290      295
122 gtt aag ctg ctg cag gtt ggg gag gaa gga cct cag gca gtg gcc aag 1083
123 Val Lys Leu Leu Gln Val Gly Glu Glu Gly Pro Gln Ala Val Ala Lys
124      300      305      310
126 ctt ctg atc aag gca tca gct gtc ctg agc aag agt atg gag gca cca 1131
127 Leu Leu Ile Lys Ala Ser Ala Val Leu Ser Lys Ser Met Glu Ala Pro
128      315      320      325
130 tca ccc cca ctt cgg gca ttg tat gag agc tgc cag ttc ttc ctt tca 1179

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131 Ser Pro Pro Leu Arg Ala Leu Tyr Glu Ser Cys Gln Phe Phe Leu Ser
132 330          335          340          345
134 ggc ctg gaa cga ggc acc aag agg cgc tat aga ctt gat gcc att ctg 1227
135 Gly Leu Glu Arg Gly Thr Lys Arg Arg Tyr Arg Leu Asp Ala Ile Leu
136          350          355          360
138 agc ctc ttt gct ttt ctt gga ggg tac tgc tct ctt ctg cag cag ctg 1275
139 Ser Leu Phe Ala Phe Leu Gly Gly Tyr Cys Ser Leu Leu Gln Gln Leu
140          365          370          375
142 cgg gat gat ggt gtg tat ggg ggc tcc tcc aag caa cag cag tct ttt 1323
143 Arg Asp Asp Gly Val Tyr Gly Gly Ser Ser Lys Gln Gln Gln Ser Phe
144          380          385          390
146 ctt cag atg tac ttt cag gga ctt cac ctc tac act gtg gtg gtt tat 1371
147 Leu Gln Met Tyr Phe Gln Gly Leu His Leu Tyr Thr Val Val Val Tyr
148          395          400          405
150 gac ttt gcc caa ggc tgt cag ata gtt gat ttg gct gac ctg acc caa 1419
151 Asp Phe Ala Gln Gly Cys Gln Ile Val Asp Leu Ala Asp Leu Thr Gln
152 410          415          420          425
154 cta gtg gac agt tgt aaa tct acc gtt gtc tgg atg ctg gag gcc tta 1467
155 Leu Val Asp Ser Cys Lys Ser Thr Val Val Trp Met Leu Glu Ala Leu
156          430          435          440
158 gag ggc ctg tgc ggc caa gag ctg acg gac cac atg ggg atg acc gct 1515
159 Glu Gly Leu Ser Gly Gln Glu Leu Thr Asp His Met Gly Met Thr Ala
160          445          450          455
162 tct tac acc agt aat ttg gcc tac agc ttc tat agt cac aag ctc tat 1563
163 Ser Tyr Thr Ser Asn Leu Ala Tyr Ser Phe Tyr Ser His Lys Leu Tyr
164          460          465          470
166 gcc gag gcc tgt gcc atc tct gag ccg ctc tgt cag cac ctg ggt ttg 1611
167 Ala Glu Ala Cys Ala Ile Ser Glu Pro Leu Cys Gln His Leu Gly Leu
168          475          480          485
170 gtg aag cca ggc act tat ccc gag gtg cct cct gag aag ttg cac agg 1659
171 Val Lys Pro Gly Thr Tyr Pro Glu Val Pro Pro Glu Lys Leu His Arg
172 490          495          500          505
174 tgc ttc cgg cta caa gta gag agt ttg aag aaa ctg ggt aaa cag gcc 1707
175 Cys Phe Arg Leu Gln Val Glu Ser Leu Lys Lys Leu Gly Lys Gln Ala
176          510          515          520
178 cag ggc tgc aag atg gtg att ttg tgg ctg gca gcc ctg caa ccc tgt 1755
179 Gln Gly Cys Lys Met Val Ile Leu Trp Leu Ala Ala Leu Gln Pro Cys
180          525          530          535
182 agc cct gaa cac atg gct gag cca gtc act ttc tgg gtt cgg gtc aag 1803
183 Ser Pro Glu His Met Ala Glu Pro Val Thr Phe Trp Val Arg Val Lys
184          540          545          550
186 atg gat gcg gcc agg gct gga gac aag gag cta cag cta aag act ctg 1851
187 Met Asp Ala Ala Arg Ala Gly Asp Lys Glu Leu Gln Leu Lys Thr Leu
188          555          560          565
190 cga gac agc ctc agt ggc tgg gac ccg gag acc ctg gcc ctc ctg ctg 1899
191 Arg Asp Ser Leu Ser Gly Trp Asp Pro Glu Thr Leu Ala Leu Leu Leu
192 570          575          580          585
195 agg gag gag ctg cag gcc tac aag gcg gtg cgg gcc gac act gga cag 1947
196 Arg Glu Glu Leu Gln Ala Tyr Lys Ala Val Arg Ala Asp Thr Gly Gln

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197		590		595		600	
199	gaa cgc ttc aac atc atc tgt gac ctc ctg gag ctg agc ccc gag gag	1995					
200	Glu Arg Phe Asn Ile Ile Cys Asp Leu Leu Glu Leu Ser Pro Glu Glu						
201		605		610		615	
203	aca cca gcc ggg gcc tgg gca cga gcc acc cac ctg gta gaa ctg gct	2043					
204	Thr Pro Ala Gly Ala Trp Ala Arg Ala Thr His Leu Val Glu Leu Ala						
205		620		625		630	
207	cag gtg ctc tgc tac cac gac ttt acg cag cag acc aac tgc tct gct	2091					
208	Gln Val Leu Cys Tyr His Asp Phe Thr Gln Gln Thr Asn Cys Ser Ala						
209		635		640		645	
211	ctg gat gct atc cgg gaa gcc ctg cag ctt ctg gac tct gtg agg cct	2139					
212	Leu Asp Ala Ile Arg Glu Ala Leu Gln Leu Leu Asp Ser Val Arg Pro						
213	650		655		660		665
215	gag gcc cag gcc aga gat cag ctt ctg gac gat aaa gca cag gcc ttg	2187					
216	Glu Ala Gln Ala Arg Asp Gln Leu Leu Asp Asp Lys Ala Gln Ala Leu						
217		670		675		680	
219	ctg tgg ctt tac atc tgt act ctg gaa gcc aaa ata cag gaa ggt atc	2235					
220	Leu Trp Leu Tyr Ile Cys Thr Leu Glu Ala Lys Ile Gln Glu Gly Ile						
221		685		690		695	
223	gag cgg gat cgg aga gcc cag gcc cct ggt aac ttg gag gaa ttt gaa	2283					
224	Glu Arg Asp Arg Arg Ala Gln Ala Pro Gly Asn Leu Glu Glu Phe Glu						
225		700		705		710	
227	gtc aat gac ctg aac tat gaa gat aaa ctc cag gaa gat cgt ttc cta	2331					
228	Val Asn Asp Leu Asn Tyr Glu Asp Lys Leu Gln Glu Asp Arg Phe Leu						
229		715		720		725	
231	tac agt aac att gcc ttc aac ctg gct gca gat gct gct cag tcc aaa	2379					
232	Tyr Ser Asn Ile Ala Phe Asn Leu Ala Ala Asp Ala Ala Gln Ser Lys						
233	730		735		740		745
235	tgc ctg gac caa gcc ctg gcc ctg tgg aag gag ctg ctt aca aag ggg	2427					
236	Cys Leu Asp Gln Ala Leu Ala Leu Trp Lys Glu Leu Leu Thr Lys Gly						
237		750		755		760	
239	cag gcc cca gct gta cgg tgt ctc cag cag aca gca gcc tca ctg cag	2475					
240	Gln Ala Pro Ala Val Arg Cys Leu Gln Gln Thr Ala Ala Ser Leu Gln						
241		765		770		775	
243	atc cta gca gcc ctc tac cag ctg gtg gca aag ccc atg cag gct ctg	2523					
244	Ile Leu Ala Ala Leu Tyr Gln Leu Val Ala Lys Pro Met Gln Ala Leu						
245		780		785		790	
247	gag gtc ctc ctg ctg cta cgg att gtc tot gag aga ctg aag gac cac	2571					
248	Glu Val Leu Leu Leu Leu Arg Ile Val Ser Glu Arg Leu Lys Asp His						
249		795		800		805	
251	tcg aag gca gct ggc tcc tcc tgc cac atc acc cag ctc ctc ctg acc	2619					
252	Ser Lys Ala Ala Gly Ser Ser Cys His Ile Thr Gln Leu Leu Leu Thr						
253	810		815		820		825
256	ctc ggc tgt ccc agc tat gcc cag tta cac ctg gaa gag gca gca tcg	2667					
257	Leu Gly Cys Pro Ser Tyr Ala Gln Leu His Leu Glu Glu Ala Ala Ser						
258		830		835		840	
260	agc ctg aag cat ctc gat cag act act gac aca tac ctg ctc ctt tcc	2715					
261	Ser Leu Lys His Leu Asp Gln Thr Thr Asp Thr Tyr Leu Leu Leu Ser						
262		845		850		855	

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264 ctg acc tgt gat ctg ctt cga agt caa ctc tac tgg act cac cag aag 2763
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266      860      865      870
268 gtg acc aag ggt gtc tct ctg ctg ctg tct gtg ctt cgg gat cct gcc 2811
269 Val Thr Lys Gly Val Ser Leu Leu Leu Ser Val Leu Arg Asp Pro Ala
270      875      880      885
272 ctc cag aag tcc tcc aag gct tgg tac ttg ctg cgt gtc cag gtc ctg 2859
273 Leu Gln Lys Ser Ser Lys Ala Trp Tyr Leu Leu Arg Val Gln Val Leu
274 890      895      900      905
276 cag ctg gtg gca gct tac ctt agc ctc ccg tca aac aac ctc tca cac 2907
277 Gln Leu Val Ala Ala Tyr Leu Ser Leu Pro Ser Asn Asn Leu Ser His
278      910      915      920
280 tcc ctg tgg gag cag ctc tgt gcc caa ggc tgg cag aca cct gag ata 2955
281 Ser Leu Trp Glu Gln Leu Cys Ala Gln Gly Trp Gln Thr Pro Glu Ile
282      925      930      935
284 gct ctc ata gac tcc cat aag ctc ctc cga agc atc atc ctc ctg ctg 3003
285 Ala Leu Ile Asp Ser His Lys Leu Leu Arg Ser Ile Ile Leu Leu Leu
286      940      945      950
288 atg ggc agt gac att ctc tca act cag aaa gca gct gtg gag aca tcg 3051
289 Met Gly Ser Asp Ile Leu Ser Thr Gln Lys Ala Ala Val Glu Thr Ser
290      955      960      965
292 ttt ttg gac tat ggt gaa aat ctg gta caa aaa tgg cag gtt ctt tca 3099
293 Phe Leu Asp Tyr Gly Glu Asn Leu Val Gln Lys Trp Gln Val Leu Ser
294 970      975      980      985
296 gag gtg ctg agc tgc tca gag aag ctg gtc tgc cac ctg ggc cgc ctg 3147
297 Glu Val Leu Ser Cys Ser Glu Lys Leu Val Cys His Leu Gly Arg Leu
298      990      995      1000
300 ggt agt gtg agt gaa gcc aag gcc ttt tgc ttg gag gcc cta aaa ctt 3195
301 Gly Ser Val Ser Glu Ala Lys Ala Phe Cys Leu Glu Ala Leu Lys Leu
302      1005      1010      1015
304 aca aca aag ctg cag ata cca cgc cag tgt gcc ctg ttc ctg gtg ctg 3243
305 Thr Thr Lys Leu Gln Ile Pro Arg Gln Cys Ala Leu Phe Leu Val Leu
306      1020      1025      1030
308 aag ggc gag ctg gag ctg gcc cgc aat gac att gat ctc tgt cag tcg 3291
309 Lys Gly Glu Leu Glu Leu Ala Arg Asn Asp Ile Asp Leu Cys Gln Ser
310      1035      1040      1045
312 gac ctg cag cag gtt ctg ttc ttg ctt gag tct tgc aca gag ttt ggt 3339
313 Asp Leu Gln Gln Val Leu Phe Leu Leu Glu Ser Cys Thr Glu Phe Gly
314 1050      1055      1060      1065
317 ggg gtg act cag cac ctg gac tct gtg aag aag gtc cac ctg cag aag 3387
318 Gly Val Thr Gln His Leu Asp Ser Val Lys Lys Val His Leu Gln Lys
319      1070      1075      1080
321 ggg aag cag cag gcc cag gtc ccc tgt cct cca cag ctc cca gag gag 3435
322 Gly Lys Gln Gln Ala Gln Val Pro Cys Pro Pro Gln Leu Pro Glu Glu
323      1085      1090      1095
325 gag ctc ttc cta aga ggc cct gct cta gag ctg gtg gcc act gtg gcc 3483
326 Glu Leu Phe Leu Arg Gly Pro Ala Leu Glu Leu Val Ala Thr Val Ala
327      1100      1105      1110
329 aag gag cct ggc ccc ata gca cct tct aca aac tcc tcc cca gtc ttg 3531

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date